

SEQUENCE LISTING

<110> Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.

<120> Immunokinases

<130> 042950wo Me/FM

<140> PCT/EP2005/050131

<141> 2005-01-13

<150> 04000847.6

<151> 2004-01-16

<150> 04017928.5

<151> 2004-07-29

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<170> PatentIn Ver. 2.1

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<211> 1785

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
PMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

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<221> CDS

<222> (1)..(1785)

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<222> (1)..(21)

<223> immunoglobulin kappa chain leader sequence

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Gly	Ser	Thr	Gly	Asp	Ser	Arg	Met	Val	Gln	Ala	Ser	Met	Arg	Ser	Pro	
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Asn	Met	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Glu	Asp	Phe	Tyr	Asp	Ile	
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gga	gag	gag	ctg	ggc	agt	ggc	cag	ttt	gcc	atc	gtg	aag	aag	tgc	cgg	192
Gly	Glu	Glu	Leu	Gly	Ser	Gly	Gln	Phe	Ala	Ile	Val	Lys	Lys	Cys	Arg	
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Glu	Lys	Ser	Thr	Gly	Leu	Glu	Tyr	Ala	Ala	Lys	Phe	Ile	Lys	Lys	Arg	
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cag	agc	cgg	gcc	agc	cgt	cgg	ggc	gtg	tgc	cgg	gag	gaa	atc	gag	cgg	288
Gln	Ser	Arg	Ala	Ser	Arg	Arg	Gly	Val	Cys	Arg	Glu	Glu	Ile	Glu	Arg	
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gag	gtg	agc	atc	ctg	cgg	cag	gtg	ctg	cac	ccc	aac	atc	atc	acg	ctg	336
Glu	Val	Ser	Ile	Leu	Arg	Gln	Val	Leu	His	Pro	Asn	Ile	Ile	Thr	Leu	
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Asn	Tyr	Leu	His	Thr	Lys	Lys	Ile	Ala	His	Phe	Asp	Leu	Lys	Pro	Glu	
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aac	atc	atg	ttg	tta	gac	aag	aat	atc	cca	att	cca	cac	atc	aag	ctg	576
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Tyr	Ile	Leu	Leu	Ser	Gly	Ala	Ser	Pro	Phe	Leu	Gly	Asp	Thr	Lys	Gln	
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Phe	Phe	Ser	Gln	Thr	Ser	Glu	Leu	Ala	Lys	Asp	Phe	Ile	Arg	Lys	Leu	
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Leu	Val	Lys	Glu	Thr	Arg	Lys	Arg	Leu	Thr	Ile	Gln	Glu	Ala	Leu	Arg	
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gca Ala	gtc Val	tat Tyr	tac Tyr 420	tgt Cys	gca Ala	aaa Lys	aag Lys	aca Thr 425	act Thr	cag Gln	act Thr	acg Thr	tgg Trp 430	ggg Gly	ttt Phe	1296
cct Pro	ttt Phe	tgg Trp 435	ggc Gly	caa Gln	ggg Gly	acc Thr	acg Thr 440	gtc Val	acc Thr	gtc Val	tcc Ser	tca Ser 445	ggt Gly	gga Gly	ggc Gly	1344
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aga Arg 530	gat Asp	ttc Phe	act Thr	ctg Leu	acc Thr	atc Ile 535	agc Ser	agt Ser	gtg Val	cag Gln	gct Ala 540	gaa Glu	gac Asp	ctt Leu	gca Ala	1632
gat Asp 545	tat Tyr	cac His	tgt Cys	gga Gly	cag Gln 550	aat Asn	tac Tyr	agg Arg	tat Tyr	ccg Pro 555	ctc Leu	acg Thr	ttc Phe	ggt Gly	gct Ala 560	1680
ggc Gly	acc Thr	aag Lys	ctg Leu	gaa Glu 565	atc Ile	aaa Lys	cgg Arg	gcg Ala	gcc Ala 570	gca Ala	ggg Gly	ccc Pro	gaa Glu	caa Gln 575	aaa Lys	1728
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 pMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

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 35 40 45

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Glu	Val	Ser	Ile	Leu	Arg	Gln	Val	Leu	His	Pro	Asn	Ile	Ile	Thr	Leu
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His	Asp	Val	Tyr	Glu	Asn	Arg	Thr	Asp	Val	Val	Leu	Ile	Leu	Glu	Leu
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Val	Ser	Gly	Gly	Glu	Leu	Phe	Asp	Phe	Leu	Ala	Gln	Lys	Glu	Ser	Leu
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Ser	Glu	Glu	Glu	Ala	Thr	Ser	Phe	Ile	Lys	Gln	Ile	Leu	Asp	Gly	Val
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Tyr	Ile	Leu	Leu	Ser	Gly	Ala	Ser	Pro	Phe	Leu	Gly	Asp	Thr	Lys	Gln
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Glu	Thr	Leu	Ala	Asn	Ile	Thr	Ala	Val	Ser	Tyr	Asp	Phe	Asp	Glu	Glu
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Ala	Lys	Pro	Gly	Ala	Ala	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr
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Leu	Ser	Cys	Lys	Ala	Ser	Glu	Asn	Val	Asp	Ser	Phe	Val	Ser	Trp	Tyr
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Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Ala	Gly	Ser	Gly	Ser	Gly
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Arg	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala
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Asp	Tyr	His	Cys	Gly	Gln	Asn	Tyr	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Ala
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Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Gly	Pro	Glu	Gln	Lys
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Leu	Ile	Ser	Glu	Asp	Leu	Asn	Ser	Ala	Val	Asp	His	His	His	His	
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 <223> immunoglobulin kappa chain leader sequence

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Gly Ser Thr Gly 20 Asp Ala Ala Gln Pro 25 Ala Met Ala Gln Val 30 Lys Leu

cag gag tca ggg act gaa ctg gca aag cct ggg gcc gca gtg aag atg 144
Gln Glu Ser 35 Gly Thr Glu Leu Ala 40 Lys Pro Gly Ala Ala 45 Val Lys Met

tcc tgc aag gct tct ggc tac acc ttt act gac tac tgg atg cac tgg 192
Ser Cys Lys 50 Ala Ser Gly Tyr 55 Thr Phe Thr Asp Tyr 60 Trp Met His Trp

gtt aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att aat 240
Val Lys Gln Arg Pro Gly 70 Gln Gly Leu Glu Trp 75 Ile Gly Tyr Ile Asn 80

cct aac act gct tat act gac tac aat cag aaa ttc aag gac aag gcc 288
Pro Asn Thr Ala Tyr 85 Thr Asp Tyr Asn Gln 90 Lys Phe Lys Asp Lys 95 Ala

aca ttg act gca gac aaa tcc tcc agc aca gcc tac atg caa ctg cgc 336
Thr Leu Thr 100 Ala Asp Lys Ser Ser 105 Thr Ala Tyr Met Gln 110 Leu Arg

agc ctg acc tct gag gat tct gca gtc tat tac tgt gca aaa aag aca 384
Ser Leu Thr 115 Ser Glu Asp Ser Ala Val Tyr Tyr Cys 125 Ala Lys Lys Thr

act cag act acg tgg ggg ttt cct ttt tgg ggc caa ggg acc acg gtc 432
Thr Gln Thr Thr Trp Gly 135 Phe Pro Phe Trp Gly 140 Gln Gly Thr Thr Val

acc gtc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc ggt 480
Thr Val Ser Ser Gly 150 Gly Gly Gly Ser Gly 155 Gly Gly Gly Ser Gly 160 Gly

ggc gga tgc gac att gtg ctg acc cag tct cca aaa tcc atg gcc atg 528
Gly Gly Ser Asp Ile Val Leu Thr Gln Ser 170 Pro Lys Ser Met Ala Met

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Ser Val Gly Glu Arg Val Thr Leu Ser 185 Cys Lys Ala Ser Glu Asn Val
180 190
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ctg	ctg	ata	tac	ggg	gcc	tcc	aac	cgg	tac	act	ggg	gtc	ccc	gat	cgc	672
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Val	Gln	Ala	Glu	Asp	Leu	Ala	Asp	Tyr	His	Cys	Gly	Gln	Asn	Tyr	Arg	
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tat	ccg	ctc	acg	ttc	ggg	gct	ggc	acc	aag	ctg	gaa	atc	aaa	cgg	gcg	816
Tyr	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala	
			260					265					270			
gcc	gca	ctc	gag	tct	aga	atg	gtc	cag	gcc	tcg	atg	agg	agc	cca	aat	864
Ala	Ala	Leu	Glu	Ser	Arg	Met	Val	Gln	Ala	Ser	Met	Arg	Ser	Pro	Asn	
		275					280					285				
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Met	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Glu	Asp	Phe	Tyr	Asp	Ile	Gly	
	290					295					300					
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Lys	Ser	Thr	Gly	Leu	Glu	Tyr	Ala	Ala	Lys	Phe	Ile	Lys	Lys	Arg	Gln	
				325					330					335		
agc	cgg	gcc	agc	cgt	cgg	ggc	gtg	tgc	cgg	gag	gaa	atc	gag	cgg	gag	1056
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Val	Ser	Ile	Leu	Arg	Gln	Val	Leu	His	Pro	Asn	Ile	Ile	Thr	Leu	His	
		355				360						365				
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Asp	Leu	Tyr	Glu	Asn	Arg	Thr	Asp	Val	Val	Leu	Ile	Leu	Glu	Leu	Val	
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Glu	Glu	Glu	Ala	Thr	Ser	Phe	Ile	Lys	Gln	Ile	Leu	Asp	Gly	Val	Asn	
				405					410					415		
tac	ctt	cac	aca	aag	aaa	att	gct	cac	ttt	gat	ctc	aag	cca	gaa	aac	1296
Tyr	Leu	His	Thr	Lys	Lys	Ile	Ala	His	Phe	Asp	Leu	Lys	Pro	Glu	Asn	
			420					425					430			
atc	atg	ttg	tta	gac	aag	aat	atc	cca	att	cca	cac	atc	aag	ctg	att	1344
Ile	Met	Leu	Leu	Asp	Lys	Asn	Ile	Pro	Ile	Pro	His	Ile	Lys	Leu	Ile	
		435					440					445				
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Asp	Phe	Gly	Leu	Ala	His	Glu	Ile	Glu	Asp	Gly	Val	Glu	Phe	Lys	Asn	
	450					455					460					

att ttt ggg aca cct gaa ttt gtt gct cca gaa atc gtg aac tat gag Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu 465 470 475 480	1440
cca ctg gga ctg gag gcc gac atg tgg agc att gga gtc atc acc tat Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr 485 490 495	1488
atc ctt cta agt gga gcg tcc ccc ttc ctg gga gac aca aaa caa gaa Ile Leu Leu Ser Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu 500 505 510	1536
acc ctg gca aat atc act gct gtg agt tac gac ttt gat gag gaa ttc Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu Phe 515 520 525	1584
ttc agc cag aca agc gag ctg gcc aag gac ttc att cgg aag ctt ctt Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu 530 535 540	1632
gtg aaa gag acc cgg aaa cgg ctt acc atc caa gag gct ctc aga cat Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His 545 550 555 560	1680
ccc tgg atc gga tcc aaa cta gct gag cac gaa ttt cga gga ggg ccc Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Phe Arg Gly Gly Pro 565 570 575	1728
gaa caa aaa ctc atc tca gaa gag gat ctg aat agc gcc gtc gac cat Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His 580 585 590	1776
cat cat cat cat cat tga His His His His His 595	1794

<210> 4
 <211> 597
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:
 pMS-(Ki-4-DAPK2')-II/G ORF

<400> 4
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu
 20 25 30
 Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met
 35 40 45
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp
 50 55 60
 Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 65 70 75 80
 Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala
 85 90 95
 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg
 100 105 110
 Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr
 115 120 125
 Thr Gln Thr Thr Trp Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val
 130 135 140
 Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 145 150 155 160
 Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met
 165 170 175
 Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val
 180 185 190

Asp	Ser	Phe	Val	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys
		195					200					205			
Leu	Leu	Ile	Tyr	Gly	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg
	210					215					220				
Phe	Ala	Gly	Ser	Gly	Ser	Gly	Arg	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser
	225				230					235					240
Val	Gln	Ala	Glu	Asp	Leu	Ala	Asp	Tyr	His	Cys	Gly	Gln	Asn	Tyr	Arg
				245					250					255	
Tyr	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala
			260					265					270		
Ala	Ala	Leu	Glu	Ser	Arg	Met	Val	Gln	Ala	Ser	Met	Arg	Ser	Pro	Asn
		275					280					285			
Met	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Glu	Asp	Phe	Tyr	Asp	Ile	Gly
	290					295					300				
Glu	Glu	Leu	Gly	Ser	Gly	Gln	Phe	Ala	Ile	Val	Lys	Lys	Cys	Arg	Glu
	305				310					315					320
Lys	Ser	Thr	Gly	Leu	Glu	Tyr	Ala	Ala	Lys	Phe	Ile	Lys	Lys	Arg	Gln
				325					330					335	
Ser	Arg	Ala	Ser	Arg	Arg	Gly	Val	Cys	Arg	Glu	Glu	Ile	Glu	Arg	Glu
			340					345					350		
Val	Ser	Ile	Leu	Arg	Gln	Val	Leu	His	Pro	Asn	Ile	Ile	Thr	Leu	His
		355					360					365			
Asp	Leu	Tyr	Glu	Asn	Arg	Thr	Asp	Val	Val	Leu	Ile	Leu	Glu	Leu	Val
	370					375					380				
Ser	Gly	Gly	Glu	Leu	Phe	Asp	Phe	Leu	Ala	Gln	Lys	Glu	Ser	Leu	Ser
	385				390					395					400
Glu	Glu	Glu	Ala	Thr	Ser	Phe	Ile	Lys	Gln	Ile	Leu	Asp	Gly	Val	Asn
				405					410					415	
Tyr	Leu	His	Thr	Lys	Lys	Ile	Ala	His	Phe	Asp	Leu	Lys	Pro	Glu	Asn
			420					425					430		
Ile	Met	Leu	Leu	Asp	Lys	Asn	Ile	Pro	Ile	Pro	His	Ile	Lys	Leu	Ile
		435					440					445			
Asp	Phe	Gly	Leu	Ala	His	Glu	Ile	Glu	Asp	Gly	Val	Glu	Phe	Lys	Asn
	450					455					460				
Ile	Phe	Gly	Thr	Pro	Glu	Phe	Val	Ala	Pro	Glu	Ile	Val	Asn	Tyr	Glu
	465				470				475						480
Pro	Leu	Gly	Leu	Glu	Ala	Asp	Met	Trp	Ser	Ile	Gly	Val	Ile	Thr	Tyr
				485					490					495	
Ile	Leu	Leu	Ser	Gly	Ala	Ser	Pro	Phe	Leu	Gly	Asp	Thr	Lys	Gln	Glu
			500					505					510		
Thr	Leu	Ala	Asn	Ile	Thr	Ala	Val	Ser	Tyr	Asp	Phe	Asp	Glu	Glu	Phe
		515					520					525			
Phe	Ser	Gln	Thr	Ser	Glu	Leu	Ala	Lys	Asp	Phe	Ile	Arg	Lys	Leu	Leu
	530					535					540				
Val	Lys	Glu	Thr	Arg	Lys	Arg	Leu	Thr	Ile	Gln	Glu	Ala	Leu	Arg	His
	545				550					555					560
Pro	Trp	Ile	Gly	Ser	Lys	Leu	Ala	Glu	His	Glu	Phe	Arg	Gly	Gly	Pro
				565					570					575	
Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Ser	Ala	Val	Asp	His
			580					585					590		
His	His	His	His												
		595													

<210> 5

<211> 3102

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PMT-Ki-4
(scFv)-eEF-2K ORF

<220>

<221> CDS

<222> (1)..(3102)

<220>

<221> N_region
 <222> (2)..(22)
 <223> pelB leader sequence

<400> 5

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Met	Lys	Tyr	Leu	Leu	Pro	Thr	Ala	Ala	Ala	Gly	Leu	Leu	Leu	Leu	Ala	
1				5					10					15		
gcc	cag	ccg	gcg	atg	gcc	atg	ggc	cat	cat	cat	cat	cat	cat	cat	cat	96
Ala	Gln	Pro	Ala	Met	Ala	Met	Gly	His	His	His	His	His	His	His	His	
			20					25					30			
cat	cac	agc	agc	ggc	cat	atc	gac	gac	gac	gac	aag	cat	atg	aag	ctt	144
His	His	Ser	Ser	Gly	His	Ile	Asp	Asp	Asp	Asp	Lys	His	Met	Lys	Leu	
		35					40					45				
atg	gcc	cag	ccg	gcc	atg	gcc	cag	gtc	aag	ctg	cag	gag	tca	ggg	act	192
Met	Ala	Gln	Pro	Ala	Met	Ala	Gln	Val	Lys	Leu	Gln	Glu	Ser	Gly	Thr	
	50					55					60					
gaa	ctg	gca	aag	cct	ggg	gcc	gca	gtg	aag	atg	tcc	tgc	aag	gct	tct	240
Glu	Leu	Ala	Lys	Pro	Gly	Ala	Ala	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	
65					70					75					80	
ggc	tac	acc	ttt	act	gac	tac	tgg	atg	cac	tgg	gtt	aaa	cag	agg	cct	288
Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	Trp	Met	His	Trp	Val	Lys	Gln	Arg	Pro	
				85					90					95		
gga	cag	ggt	ctg	gaa	tgg	att	gga	tac	att	aat	cct	aac	act	gct	tat	336
Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn	Pro	Asn	Thr	Ala	Tyr	
			100					105					110			
act	gac	tac	aat	cag	aaa	ttc	aag	gac	aag	gcc	aca	ttg	act	gca	gac	384
Thr	Asp	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Ala	Asp	
		115					120					125				
aaa	tcc	tcc	agc	aca	gcc	tac	atg	caa	ctg	cgc	agc	ctg	acc	tct	gag	432
Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Arg	Ser	Leu	Thr	Ser	Glu	
	130					135					140					
gat	tct	gca	gtc	tat	tac	tgt	gca	aaa	aag	aca	act	cag	act	acg	tgg	480
Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Lys	Thr	Thr	Gln	Thr	Thr	Trp	
145					150					155					160	
ggg	ttt	cct	ttt	tgg	ggc	caa	ggg	acc	acg	gtc	acc	gtc	tcc	tca	ggt	528
Gly	Phe	Pro	Phe	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	
				165					170					175		
gga	ggc	ggt	tca	ggc	gga	ggt	ggc	tct	ggc	ggt	ggc	gga	tcg	gac	att	576
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	
			180					185					190			
gtg	ctg	acc	cag	tct	cca	aaa	tcc	atg	gcc	atg	tca	gtc	gga	gag	agg	624
Val	Leu	Thr	Gln	Ser	Pro	Lys	Ser	Met	Ala	Met	Ser	Val	Gly	Glu	Arg	
		195					200					205				
gtc	acc	ttg	agc	tgc	aag	gcc	agt	gag	aat	gtg	gat	tct	ttt	gtt	tcc	672
Val	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Glu	Asn	Val	Asp	Ser	Phe	Val	Ser	
	210					215					220					
tgg	tat	caa	cag	aaa	cca	ggc	cag	tct	cct	aaa	ctg	ctg	ata	tac	ggg	720
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Gly	
225					230					235					240	
gcc	tcc	aac	cgg	tac	act	ggg	gtc	ccc	gat	cgc	ttc	gca	ggc	agt	gga	768
Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Ala	Gly	Ser	Gly	
				245					250					255		

tct Ser	gga Gly	aga Arg	gat Asp 260	ttc Phe	act Thr	ctg Leu	acc Thr	atc Ile 265	agc Ser	agt Ser	gtg Val	cag Gln	gct Ala 270	gaa Glu	gac Asp	816
ctt Leu	gca Ala	gat Asp 275	tat Tyr	cac His	tgt Cys	gga Gly	cag Gln 280	aat Asn	tac Tyr	agg Arg	tat Tyr	ccg Pro 285	ctc Leu	acg Thr	ttc Phe	864
ggt Gly	gct Ala 290	ggc Gly	acc Thr	aag Lys	ctg Leu	gaa Glu 295	atc Ile	aaa Lys	cgg Arg	gcg Ala	gcc Ala 300	gca Ala	gag Glu	ctc Leu	ggc Gly	912
gga Gly 305	ggt Gly	ggc Gly	tct Ser	atg Met	gca Ala 310	gac Asp	gaa Glu	gat Asp	ctc Leu	atc Ile 315	ttc Phe	cgc Arg	ctg Leu	gaa Glu	ggc Gly 320	960
gtt Val	gat Asp	ggc Gly	ggc Gly	cag Gln 325	tcc Ser	ccc Pro	cga Arg	gct Ala	ggc Gly 330	cat His	gat Asp	ggt Gly	gat Asp	tct Ser 335	gat Asp	1008
ggg Gly	gac Asp	agc Ser	gac Asp 340	gat Asp	gag Glu	gaa Glu	ggt Gly	tac Tyr 345	ttc Phe	atc Ile	tgc Cys	ccc Pro	atc Ile 350	acg Thr	gat Asp	1056
gac Asp	cca Pro	agc Ser 355	tcg Ser	aac Asn	cag Gln	aat Asn	gtc Val 360	aat Asn	tcc Ser	aag Lys	gtt Val	aat Asn 365	aag Lys	tac Tyr	tac Tyr	1104
agc Ser	aac Asn 370	cta Leu	aca Thr	aaa Lys	agt Ser	gag Glu 375	cgg Arg	tat Tyr	agc Ser	tcc Ser	agc Ser 380	ggg Gly	tcc Ser	ccg Pro	gca Ala	1152
aac Asn 385	tcc Ser	ttc Phe	cac His	ttc Phe	aag Lys 390	gaa Glu	gcc Ala	tgg Trp	aag Lys	cac His 395	gca Ala	atc Ile	cag Gln	aag Lys	gcc Ala 400	1200
aag Lys	cac His	atg Met	ccc Pro	gac Asp 405	ccc Pro	tgg Trp	gct Ala	gag Glu	ttc Phe 410	cac His	ctg Leu	gaa Glu	gat Asp	att Ile 415	gcc Ala	1248
acc Thr	gaa Glu	cgt Arg	gct Ala 420	act Thr	cga Arg	cac His	agg Arg	tac Tyr 425	aac Asn	gcc Ala	gtc Val	acc Thr	ggg Gly 430	gaa Glu	tgg Trp	1296
ctg Leu	gat Asp	gat Asp 435	gaa Glu	gtt Val	ctg Leu	atc Ile	aag Lys 440	atg Met	gca Ala	tct Ser	cag Gln	ccc Pro 445	ttc Phe	ggc Gly	cga Arg	1344
gga Gly	gca Ala 450	atg Met	agg Arg	gag Glu	tgc Cys	ttc Phe 455	cgg Arg	acg Thr	aag Lys	aag Lys	ctc Leu 460	tcc Ser	aac Asn	ttc Phe	ttg Leu	1392
cat His 465	gcc Ala	cag Gln	cag Gln	tgg Trp	aag Lys 470	ggc Gly	gcc Ala	tcc Ser	aac Asn	tac Tyr 475	gtg Val	gcg Ala	aag Lys	cgc Arg	tac Tyr 480	1440
atc Ile	gag Glu	ccc Pro	gta Val	gac Asp 485	cgg Arg	gat Asp	gtg Val	tac Tyr	ttt Phe 490	gag Glu	gac Asp	gtg Val	cgt Arg	cta Leu 495	cag Gln	1488
atg Met	gag Glu	gcc Ala	aag Lys 500	ctc Leu	tgg Trp	ggg Gly	gag Glu 505	tat Tyr	aat Asn	cgg Arg	cac His	aag Lys 510	ccc Pro	ccc Pro		1536
aag Lys	cag Gln	gtg Val 515	gac Asp	atc Ile	atg Met	cag Gln	atg Met 520	tgc Cys	atc Ile	atc Ile	gag Glu	ctg Leu 525	aag Lys	gac Asp	aga Arg	1584
ccg Gly	ggc Gly	aag Arg	ccc Pro	ctc Leu	ttc Phe	cac His	ctg Leu	gag Glu	cac His	tac Tyr	atc Ile	gag Glu	ggc Gly	aag Arg	tac Tyr	1632

Pro 530	Gly	Lys	Pro	Leu	Phe	His 535	Leu	Glu	His	Tyr	Ile 540	Glu	Gly	Lys	Tyr	
atc Ile 545	aag Lys	tac Tyr	aac Asn	tcc Ser	aac Asn 550	tct Ser	ggc Gly	ttt Phe	gtc Val	cgc Arg 555	gat Asp	gac Asp	aac Asn	atc Ile	cgc Arg 560	1680
ctg Leu	acg Thr	ccg Pro	cag Gln	gcc Ala 565	ttc Phe	agc Ser	cac His	ttc Phe	act Thr 570	ttt Phe	gag Glu	cgt Arg	tcc Ser	ggc Gly 575	cat His	1728
cag Gln	ctg Leu	ata Ile	gtg Val 580	gtg Val	gac Asp	atc Ile	cag Gln	gga Gly 585	gtt Val	ggg Gly	gat Asp	ctc Leu	tac Tyr 590	act Thr	gac Asp	1776
cca Pro	cag Gln	atc Ile 595	cac His	acg Thr	gag Glu	acg Thr	ggc Gly 600	act Thr	gac Asp	ttt Phe	gga Gly	gac Asp 605	ggc Gly	aac Asn	cta Leu	1824
ggc Gly 610	gtc Val	cgc Arg	ggg Gly	atg Met	gag Ala	ctc Leu 615	ttc Phe	ttc Phe	tac Tyr	tct Ser	cat His 620	gcc Ala	tgc Cys	aac Asn	cgg Arg	1872
att Ile 625	tgc Cys	gag Glu	agc Ser	atg Met	ggc Gly 630	ctt Leu	gct Ala	ccc Pro	ttt Phe	gac Asp 635	ctc Leu	tcg Ser	ccc Pro	cgg Arg	gag Glu 640	1920
agg Arg	gat Asp	gca Ala	gtg Val	aat Asn 645	cag Gln	aac Asn	acc Thr	aag Lys	ctg Leu 650	ctg Leu	caa Gln	tca Ser	gcc Ala	aag Lys 655	acc Thr	1968
atc Ile	ttg Leu	aga Arg	gga Gly 660	aca Thr	gag Glu	gaa Glu	aaa Lys	tgt Cys 665	ggg Gly	agc Ser	ccc Pro	cga Arg	gta Val 670	agg Arg	acc Thr	2016
ctc Leu	tct Ser	ggg Gly 675	agc Ser	cgg Arg	cca Pro	ccc Pro	ctg Leu 680	ctc Leu	cgt Arg	ccc Pro	ctt Leu	tca Ser 685	gag Glu	aac Asn	tct Ser	2064
gga Gly 690	gac Asp	gag Glu	aac Asn	atg Met	agc Ser	gac Asp 695	gtg Val	acc Thr	ttc Phe	gac Asp	tct Ser 700	ctc Leu	cct Pro	tct Ser	tcc Ser	2112
cca Pro 705	tct Ser	tcg Ser	gcc Ala	aca Thr	cca Pro 710	cac His	agc Ser	cag Gln	aag Lys	cta Leu 715	gac Asp	cac His	ctc Leu	cat His	tgg Trp 720	2160
cca Pro	gtc Val	ttc Phe	agt Ser	gac Asp 725	ctc Leu	gat Asp	aac Asn	atg Met	gca Ala 730	tcc Ser	aga Arg	gac Asp	cat His	gat Asp 735	cat His	2208
cta Leu	gac Asp	aac Asn	cac His 740	cgg Arg	gag Glu	tct Ser	gag Glu	aat Asn 745	agt Ser	ggg Gly	gac Asp	agc Ser	gga Gly 750	tac Tyr	ccc Pro	2256
agt Ser	gag Glu	aag Lys 755	cgg Arg	ggt Gly	gag Glu	ctg Leu	gat Asp 760	gac Asp	cct Pro	gag Glu	ccc Pro	cga Arg 765	gaa Glu	cat His	ggc Gly	2304
cac His	tca Ser 770	tac Tyr	agt Ser	aat Asn	cgg Arg	aag Lys 775	tac Tyr	gag Glu	tct Ser	gac Asp	gaa Glu 780	gac Asp	agc Ser	ctg Leu	ggc Gly	2352
agc Ser 785	tct Ser	gga Gly	cgg Arg	gta Val	tgt Cys 790	gta Val	gag Glu	aag Lys	tgg Trp	aat Asn 795	ctc Leu	ctc Leu	aac Asn	tcc Ser	tcc Ser 800	2400
cgc Arg	ctc Leu	cac His	ctg Leu	ccg Pro	agg Arg	gct Ala	tcg Ser	gcc Ala	gtg Val	gcc Ala	ctg Leu	gaa Glu	gtg Val	caa Gln	agg Arg	2448

805										810					815					
ctt	aat	gct	ctg	gac	ctc	gaa	aag	aaa	atc	ggg	aag	tcc	att	ttg	ggg	2496				
Leu	Asn	Ala	Leu	Asp	Leu	Glu	Lys	Lys	Ile	Gly	Lys	Ser	Ile	Leu	Gly					
			820					825					830							
aag	gtc	cat	ctg	gcc	atg	gtg	cgc	tac	cac	gag	ggt	ggg	cgc	ttc	tgc	2544				
Lys	Val	His	Leu	Ala	Met	Val	Arg	Tyr	His	Glu	Gly	Gly	Arg	Phe	Cys					
		835					840					845								
gag	aag	ggc	gag	gag	tgg	gac	cag	gag	tcg	gct	gtc	ttc	cac	ctg	gag	2592				
Glu	Lys	Gly	Glu	Glu	Trp	Asp	Gln	Glu	Ser	Ala	Val	Phe	His	Leu	Glu					
	850					855					860									
cac	gca	gcc	aac	ctg	ggc	gag	ctg	gag	gcc	atc	gtg	ggc	ctg	gga	ctc	2640				
His	Ala	Ala	Asn	Leu	Gly	Glu	Leu	Glu	Ala	Ile	Val	Gly	Leu	Gly	Leu					
					870					875					880					
atg	tac	tcg	cag	ttg	cct	cat	cac	atc	cta	gcc	gat	gtc	tct	ctg	aag	2688				
Met	Tyr	Ser	Gln	Leu	Pro	His	His	Ile	Leu	Ala	Asp	Val	Ser		Lys					
				885					890					895						
gag	aca	gaa	gag	aac	aaa	acc	aaa	gga	ttt	gat	tac	tta	cta	aag	gcc	2736				
Glu	Thr	Glu	Glu	Asn	Lys	Thr	Lys	Gly	Phe	Asp	Tyr	Leu	Leu	Lys	Ala					
			900					905					910							
gct	gaa	gct	ggc	gac	agg	cag	tcc	atg	atc	cta	gtg	gcg	cga	gct	ttt	2784				
Ala	Glu	Ala	Gly	Asp	Arg	Gln	Ser	Met	Ile	Leu	Val	Ala	Arg	Ala	Phe					
		915					920					925								
gac	tct	ggc	cag	aac	ctc	agc	ccg	gac	agg	tgc	caa	gac	tgg	cta	gag	2832				
Asp	Ser	Gly	Gln	Asn	Leu	Ser	Pro	Asp	Arg	Cys	Gln	Asp	Trp	Leu	Glu					
	930					935					940									
gcc	ctg	cac	tgg	tac	aac	act	gcc	ctg	gag	atg	acg	gac	tgt	gat	gag	2880				
Ala	Leu	His	Trp	Tyr	Asn	Thr	Ala	Leu	Glu	Met	Thr	Asp	Cys	Asp	Glu					
					950					955					960					
ggc	ggt	gag	tac	gac	gga	atg	cag	gac	gag	ccc	cgg	tac	atg	atg	ctg	2928				
Gly	Gly	Glu	Tyr	Asp	Gly	Met	Gln	Asp	Glu	Pro	Arg	Tyr	Met	Met	Leu					
				965					970					975						
gcc	agg	gag	gcc	gag	atg	ctg	ttc	aca	gga	ggc	tac	ggg	ctg	gag	aag	2976				
Ala	Arg	Glu	Ala	Glu	Met	Leu	Phe	Thr	Gly	Gly	Tyr	Gly	Leu	Glu	Lys					
			980					985					990							
gac	ccg	cag	aga	tca	ggg	gac	ttg	tat	acc	cag	gca	gca	gag	gca	gcg	3024				
Asp	Pro	Gln	Arg	Ser	Gly	Asp	Leu	Tyr	Thr	Gln	Ala	Ala	Glu	Ala	Ala					
		995					1000				1005									
atg	gaa	gcc	atg	aag	ggc	cga	ctg	gcc	aac	cag	tac	tac	caa	aag	gct	3072				
Met	Glu	Ala	Met	Lys	Gly	Arg	Leu	Ala	Asn	Gln	Tyr	Tyr	Gln	Lys	Ala					
	1010					1015					1020									
gaa	gag	gcc	tgg	gcc	cag	atg	gag	gag	taa							3102				
Glu	Glu	Ala	Trp	Ala	Gln	Met	Glu	Glu												
	1025				1030															

<210> 6

<211> 1033

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: PMT-Ki-4
(scFv)-eEF-2K ORF

<400> 6

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala	Gln	Pro	Ala	Met	Ala	Met	Gly	His	His	His	His	His	His	His	His	His
His	His	Ser	Ser	Gly	His	Ile	Asp	Asp	Asp	Asp	Lys	His	Met	Lys	Leu	
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Thr	Asp	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Ala	Asp	
Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Arg	Ser	Leu	Thr	Ser	Glu	
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Ser	Asn	Leu	Thr	Lys	Ser	Glu	Arg	Tyr	Ser	Ser	Ser	Gly	Ser	Pro	Ala	
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Lys	His	Met	Pro	Asp	Pro	Trp	Ala	Glu	Phe	His	Leu	Glu	Asp	Ile	Ala	
Thr	Glu	Arg	Ala	Thr	Arg	His	Arg	Tyr	Asn	Ala	Val	Thr	Gly	Glu	Trp	
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Leu	Thr	Pro	Gln	Ala	Phe	Ser	His	Phe	Thr	Phe	Glu	Arg	Ser	Gly	His	

Gln	Leu	Ile	Val	565 Val	Asp	Ile	Gln	Gly	570 Val	Gly	Asp	Leu	Tyr	575 Thr	Asp
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Ile	Cys	Glu	Ser	Met	Gly	Leu	615 Ala	Pro	Phe	Asp	Leu	Ser	Pro	Arg	Glu
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Gly	Asp	Glu	Asn	Met	Ser	Asp	680 Val	Thr	Phe	Asp	Ser	Leu	685 Pro	Ser	Ser
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705 Pro	Val	Phe	Ser	Asp	710 Leu	Asp	Asn	Met	Ala	715 Ser	Arg	Asp	His	Asp	His
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Ala	Glu	Ala	Gly	Asp	Arg	Gln	Ser	905 Met	Ile	Leu	Val	Ala	Arg	Ala	Phe
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Ala	Leu	His	Trp	Tyr	Asn	Thr	Ala	Leu	Glu	Met	Thr	Asp	Cys	Asp	Glu
945 Gly	Gly	Glu	Tyr	Asp	Gly	Met	Gln	Asp	Glu	Pro	Arg	Tyr	Met	Met	Leu
Ala	Arg	Glu	Ala	Glu	Met	Leu	Phe	Thr	Gly	Gly	Tyr	Gly	Leu	Glu	Lys
Asp	Pro	Gln	Arg	Ser	Gly	Asp	Leu	Tyr	Thr	Gln	Ala	Ala	Glu	Ala	Ala
Met	Glu	Ala	Met	Lys	Gly	Arg	Leu	Ala	Asn	Gln	Tyr	Tyr	Gln	Lys	Ala
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linker

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